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Abstract

Ichthyop is a free Java tool designed to study the effects of physical and biological factors on ichthyoplankton dynamics. It incorporates the most important processes involved in fish early life: spawning, movement, growth, mortality and recruitment. The tool uses as input time series of velocity, temperature and salinity fields archived from ROMS or MARS oceanic models. It runs with a user-friendly graphic interface and generates output files that can be post-processed easily using graphic and statistical software.

Keywords

Ichthyop; Biophysical model; Lagrangian model; Individual-based model; Particle tracking; Fish early life; Fish eggs and larvae; Transport.

Software availability

Name of software Ichthyop

Developer Verley Philippe

Contact details info@previmer.org

Hardware required Pentium IV and 512 Mb of RAM memory advised

Software required Java Runtime Environment (JRE) 1.6v or above

Program language Java

Program size ~ 12 Mb

Availability and cost free software declared under GPL license, download from http://www.ur097.ird.fr/projects/ichthyop/

Introduction

The dynamics of ichthyoplankton (fish eggs and larvae) is heavily influenced by advective processes. These processes largely determine the transport of ichthyoplankton within the system, and therefore the environmental conditions that it experiences. Many models coupling physics with ichthyoplankton dynamics have been developed (reviewed in Miller 2007). To our knowledge, the computer implementations of these models are however not easily

available, and certainly not as user-friendly tools. There is an ongoing effort to structure the community who uses such models. A recent example is the "Workshop on advancements in modeling physical-biological interactions in fish early-life history: recommended practices and future directions" (Gallego et al. 2007). Sharing tools also helps to structure a community. We developed the Ichthyop tool with this idea in mind.

The tool

Ichthyop has been developed to study how physical (e.g., ocean currents, temperature) and biological (e.g., growth, mortality) factors affect the dynamics of ichthyoplankton. The tool uses time series of velocity, temperature and salinity fields archived from oceanic simulations of the "Regional Oceanic Modelling System" (ROMS, Shchepetkin and McWilliams 2005) or the "Model for Applications at Regional Scale" (MARS, Lazure and Dumas 2008). It also enables to track virtual drifters and the ocean properties (temperature, salinity) that they experience.

Ichthyop is a free Java tool that can be downloaded from http://www.ur097.ird.fr/projects/ichthyop/. A Java Runtime Environment (JRE) is needed to run it. The distributed package consists of a compressed archive (~ 12 Mb) that contains the program source code, byte code, libraries, and an example of ROMS simulation allowing first-time users to run the program. A user guide (pdf format, ~ 0.7 Mb) is also provided.

Ichthyop offers two functioning modes. The first one allows a visualization of the transport of virtual eggs and larvae in a user-friendly graphic interface (Figure 1). The second mode

enables to run series of simulations based on pre-defined sets of parameters, with a minimalist interface.

Figure 1

The tool is a generic version of previous modelling experiments investigating the effects of physical and biological factors on the dynamics of anchovy and sardine ichthyoplankton in the Benguela (Mullon et al. 2002, Huggett et al. 2003, Mullon et al. 2003, Parada et al. 2003, Lett et al. 2006, Miller et al. 2006, Lett et al. 2007b) and in the Humboldt (Lett et al. 2007a, Brochier et al. submitted) upwelling systems.

The model

The model description follows the Overview-Design-Details (ODD) protocol for describing individual- and agent-based models (Grimm et al. 2006) and consists of seven elements. The first three elements provide an overview, the fourth element explains general concepts underlying the model's design, and the remaining three elements provide details.

Purpose

Ichthyop is an individual-based model (IBM) designed to study the effects of physical and biological factors on the dynamics of fish eggs and larvae.

State variables and scales

The IBM comprises individuals and their physical environment. Individuals are characterized by the state variables: age [day], length [mm], stage (egg, yolk-sac larva or feeding larva), location (longitude [°E], latitude [°N] and depth [m]) and status (alive or dead). The physical environment is characterized by ocean state variables: current velocities [$m.s^{-1}$], temperature [°C] and salinity.

The environment state variables are provided on a discrete three-dimensional grid by archived simulations of the ROMS or MARS oceanic models. As an example of typical spatial scales used to characterize the environment, we describe the ROMS southern Benguela configuration grid (Penven et al. 2001) It extends from 28 to 40° S and from 10 to 24° E. The horizontal resolution ranges from 9 km at the coast to 16 km offshore. The vertical resolution ranges from 1 to 4.7 m at the surface and from 3.1 to 1030 m at the bottom of the ocean.

The IBM sees the Eulerian velocity field at the same spatial scale as the Eulerian primitive equation models (ROMS/MARS). Subgriscale parameterizations can be added in the IBM to address scales unresolved by the primitive equation models (see the dispersion terms in the IBM movement submodel below).

In ROMS, the current velocities, temperature and salinity fields are typically averaged over time and stored every day or so. In the IBM, these fields are interpolated in space to provide values at any individual location. They are also interpolated in time to feed the IBM time step (typically one hour). Simulations consist in tracking the locations and properties of the individuals (typically during a few weeks or months).

Process overview and scheduling

After initialization (spawning), the IBM proceeds in discrete time steps. Within each time step each individual moves, grows and tests for mortality and recruitment. The spawning, movement, growth, mortality and recruitment submodels are described below. The environment state variables are updated during the simulation at a frequency equal to that of the ROMS/MARS stored outputs.

Design concepts

Stochasticity. The release location of each individual is chosen randomly within the specified spawning areas. This is used to simulate patchy or uniform distributions depending on a patchiness parameter (see the spawning submodel below). The horizontal and vertical dispersion components of the movement (see the movement submodel below) are also stochastic.

Observation. The advection part of the movement submodel has been tested by recording trajectories of individuals and comparing them to trajectories obtained using two other Lagrangian tools ("Roff", Capet et al. 2004, Carr et al. 2008, http://www.atmos.ucla.edu/~capet/Myresearch/my_research_floats.html; "Ariane", Blanke and Raynaud 1997, Blanke et al. 1999, http://www.univ-brest.fr/lpo/ariane). The present tool offers two functioning modes (a graphic interface and a serial mode, see "The tool" section above) and associated observation modes (output files, see "The simulations" section below).

Initialization

The IBM first loads a configuration file (see "The simulations" section below). Then individuals are released according to a spawning strategy set by the user (see the spawning submodel below), at the egg stage, with an initial length of 0.025 mm.

Input

The fields of environment state variables are the input of the IBM. They are provided by archived simulations of ROMS or MARS.

Submodels

Spawning. The spawning strategy is defined by the user. The tool offers two modes for releasing eggs. The first one, zone release, implies setting the number of eggs and the spawning areas, depth, frequency and patchiness. Each spawning area is defined by the coordinates (longitude [°E], latitude [°N]) of four points and by two bathymetric lines [m]. The four points delimit a polygon and the spawning area is set as the portion of the polygon contained between the bathymetric lines. Depth of spawning is defined by upper and lower depth levels [m]. Spawning begins at the beginning of the simulation. There may be several spawning events: the number of spawning events and the time between two events are set by the user. Eggs may be released by patches inside the spawning areas: the user defines the number of patches, their radius (horizontal dimension [m]) and thickness (vertical dimension [m]). The alternative release mode allows reading the initial location of the released individuals from input files (see the Ichthyop user guide).

Movement. The movement submodel simulates the following processes: horizontal advection, vertical advection, horizontal dispersion, vertical dispersion, egg buoyancy and larval vertical migration. Horizontal advection is always used in the movement equation. Vertical advection is always used too, except at the larval stage if the user chooses to apply the vertical migration scheme instead. The vertical migration scheme implemented is diel vertical migration where larvae spend daytime and night-time at user-specified depths. Daytime begins at 7 a.m. and night-time at 7 p.m. A user who wants to change these values or to consider another vertical migration scheme will have to make changes in this submodel (see the Ichthyop user guide). The user can choose to apply a buoyancy scheme at the egg stage. When buoyancy is taken into account a term is added to the vertical velocity. This term depends on the difference between egg density and water density. Egg density [$g.cm^{-3}$] is a parameter chosen by the user and water density is a function of temperature and salinity. For a complete description of the buoyancy scheme we refer to Parada et al. (2003). The user can also choose to apply horizontal dispersion and vertical dispersion. Horizontal dispersion has been implemented following Peliz et al. (2007). A random displacement model has been implemented for vertical dispersion (Visser 1997), using a cubic spline interpolation of the vertical diffusivity fields read in the environment state variables. For time-stepping a forward-Euler or a 4^{th} order Runge-Kutta integration schemes can be used.

Growth. Length l [mm] increases linearly with time t [day] (eq. 1a), at a rate r taken as a linear function of temperature T [°C] (eq. 1b).

$$l(t+\Delta t) = l(t) + r\Delta t \tag{1a}$$

$$r = 0.02 + 0.03T \tag{1b}$$

Individuals change stages according to their length, going from egg to yolk-sac larva at 2.8 mm, and from yolk-sac larva to feeding larva at 4.5 mm. These values and equations (1) are used to simulate the growth of anchovy in the southern Benguela upwelling system. A user who wants to consider another species or location may have to make changes in this submodel (see the Ichthyop user guide).

If plankton concentrations are provided in the environment state variables used in Ichthyop (e.g., they result from simulations of a NPZD biogeochemical model coupled to ROMS, Koné et al. 2005), the user may choose to apply, at the feeding larvae stage, a growth function limited by food (eq. 2):

$$r = \frac{Food}{K_s + Food}(0.02 + 0.03T) \qquad (2)$$

where K_s is a half saturation constant and $Food$ a function of phytoplankton and zooplankton concentrations (Koné 2006) that can be specified in the source code.

Mortality. Individuals die when they are in waters at a temperature below a certain value. This value of lethal temperature [°C] may be different for eggs and for larvae, and is user-specified.

Recruitment. Individuals are considered as recruited when they have reached a minimum length (or age) and spent a minimum amount of time within a "recruitment area". Recruitment areas are defined in the same way as spawning areas (see the spawning submodel above). The

minimum length (or age) at recruitment and the minimum duration of stay within recruitment areas are determined by the user.

The Simulations

Simulations are performed using either the graphic interface (SINGLE) mode of the tool or its series of simulations (SERIAL) mode. Which of these two modes is used depends on the value of the "*run*" field in the configuration file.

Configuration files. Configuration files enable the user to specify the conditions under which simulations are performed. As part of the Ichthyop tool a configuration editor helps designing configuration files for the SINGLE mode. Configuration files for the SERIAL mode have to be designed using a text editor. Basic examples of SINGLE and SERIAL configuration files are provided in the tool. We refer to the Ichthyop user guide for details about configuration files.

Output files. Output files are screen snapshots (Figure 1) in the SINGLE mode, and NetCDF files in both SINGLE and SERIAL modes. In the NetCDF output files are recorded the state variables of all individuals and of the environment they experience. We refer to the Ichthyop user guide for details about these output files. They can be post-processed easily using graphic and statistical software. Routines in R (Hornik 2007) for plotting trajectories of individuals or for computing the number of individuals transported from spawning areas to recruitment areas can be sent upon request.

Conclusion

Ichthyop is a tool designed to be shared within the community using models coupling physics with ichthyoplankton dynamics. Though it has been historically developed to study the dynamics of small pelagic fish ichthyoplankton in upwelling systems, Ichthyop is a generic tool in the sense that it incorporates the most important processes involved in ichthyoplankton dynamics. Using Ichthyop for other species in other systems may imply a few changes in the source code (e.g., changing the growth function, implementing a specific larval vertical migration scheme, etc.). This code is organized simply, commented and documented, which should make it easy to modify by a user with basic programming skills.

Acknowledgements

We are grateful to PREVIMER for financial support. We also thank Franck Dumas, John Field, Pierre Garreau, Fabrice Lecornu and Claude Roy, and three anonymous reviewers for their helpful comments.

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Figures

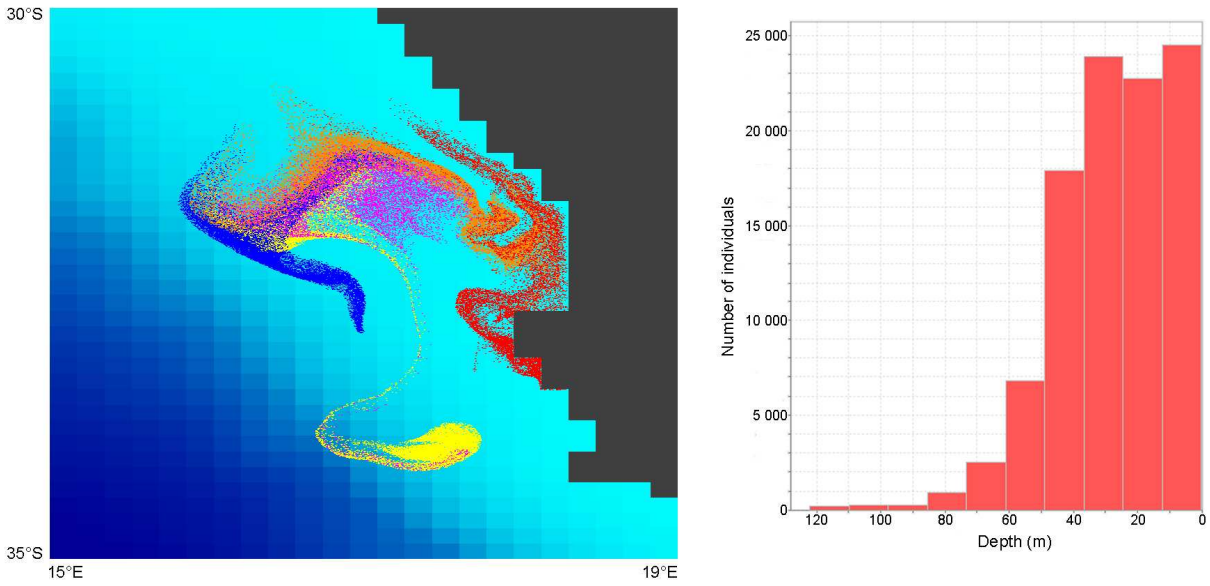

Figure 1: The simulated eggs and larvae dispersal pattern is displayed on a longitude-latitude plot in the main frame of the graphic user interface (GUI). A snapshot (with individuals coloured according to the area where they were released) is shown in the left panel. Control graphs, like the one in the right panel (showing the depth distribution of individuals), can be added in the GUI.